

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:40:52 ; Search time 16.74 seconds

(without alignments)
650.731 Million cell updates/sec

Title: US-09-483-543a-8

Perfect score: 1693
Sequence: 1 KRGCAGNDEFSERSWYGR.....QQNPDEDFSGCGXGLEVLFLQ 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	95.2	304	1	CRK_MOUSE
2	1605	94.8	304	1	CRK_RAT
3	1588	93.8	304	1	CRK_HUMAN
4	1379.5	81.5	305	1	CRK_CHICK
5	1315	77.7	296	1	CRK_XENLA
6	917.5	54.2	303	1	CRKL_HUMAN
7	911.5	53.8	303	1	CRKL_MOUSE
8	818.5	48.3	440	1	GAGC_AYISC
9	642.5	38.0	271	1	CRK_DROME
10	257	15.2	217	1	GRAP_HUMAN
11	236	13.9	211	1	DRK_DROME
12	224	13.2	217	1	GRB2_HUMAN
13	224	13.2	217	1	GRB2_MOUSE
14	218	12.9	217	1	GRB2_CHICK
15	214	12.6	217	1	GRB2_XENLA
16	202	11.9	228	1	SEM5_CAEEL
17	184	10.9	1291	1	PIG1_BOVIN
18	178	10.5	1290	1	PIG1_HUMAN
19	177	10.5	1290	1	PIG1_RAT
20	174.5	10.3	322	1	GRP2_MOUSE
21	174	10.3	845	1	VAV_HUMAN
22	173	10.2	843	1	VAV_RAT
23	167	9.9	845	1	VAV_MOUSE
24	159.5	9.4	847	1	VAV3_HUMAN
25	158.5	9.4	330	1	GRP2_HUMAN
26	157	9.3	520	1	ITSN_HUMAN
27	155.5	9.2	847	1	VAV3_MOUSE
28	154.5	9.1	878	1	VAV2_HUMAN
29	151	8.9	1168	1	MYSC_AJACA
30	150	8.9	960	1	DIGL_DROME
31	148.5	8.8	868	1	VAV2_MOUSE
32	148.5	8.8	1113	1	MYSD_DICDI
33	147	8.7	1044	1	GRPA_BOVIN

34	146.5	8.7	1038	1	GRPA_RAT	P50904	rattus norv
35	146	8.6	946	1	RHGA_HUMAN	P98171	homo sapien
36	144.5	8.5	1047	1	GRPA_HUMAN	P20936	homo sapien
37	142	8.4	450	1	CSK_CHICK	P41239	gallus gall
38	139	8.2	359	1	YKA7_CAEEL	P34258	gallus gall
39	139	8.2	1196	1	ABU1_CAEEL	P03949	caenorhabdi
40	138.5	8.2	505	1	SRK1_SPOLA	P42686	spongilla 1
41	138.5	8.2	1265	1	PIG2_RAT	P24135	rattus norv
42	138	8.2	583	1	SHC_HUMAN	P29353	homo sapien
43	137.5	8.1	578	1	SHC_MOUSE	P98083	mus musculu
44	136	8.0	450	1	CSK_HUMAN	P41240	homo sapien
45	134	7.9	450	1	CSK_MOUSE	P41241	mus musculu

ALIGNMENTS

RESULT	ID	CRK_MOUSE	STANDARD:	PRT:	304 AA.
AC	064010;	CRK_MOUSE	064010;		
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	PROTO-ONCOGENE C-CRK (P38) (ADAPTER MOLECULE CRK).				
GN	CRK OR CRKO.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=94239744; PubMed=8183562;				
RA	Ogawa S., Toyoshima H., Kozutsumi H., Hagiwara K., Sakai R., Tanaka T., Hirano N., Mano H., Yazaki Y., Hirai H.;				
RT	"The C-terminal SH3 domain of the mouse c-crk protein negatively regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1 cells.";				
RT	Oncogene 9:1669-1678(1994).				
RL	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 134-190.				
RX	MEDLINE=95253821; PubMed=7735837;				
RA	Wu X., Knudsen B., Feller S.M., Zheng J., Sali A., Cowburn D., Hanafusa H., Kuriyan J.;				
RT	"Structural basis for the specific interaction of lysine-containing proline-rich peptides with the N-terminal SH3 domain of c-Crk.";				
RT	Structure 3:215-226(1995).				
RL	[3]				
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 133-191.				
RX	MEDLINE=99069628; PubMed=9851931;				
RA	Nguyen J.T., Turk C.W., Cohen F.E., Zuckermann R.N., Lim W.A.;				
RT	"Exploiting the basis of proline recognition by SH3 and WW domains: design of N-substituted inhibitors.";				
RT	Science 282:2088-2092(1998).				
RL	-1- FUNCTION: THE CRK-I AND CRK-II FORMS DIFFER IN THEIR BIOLOGICAL ACTIVITIES. CRK-II HAS LESS TRANSFORMING ACTIVITY THAN CRK-I. BOTH CRK-I AND CRK-II BIND TO MANY OF TYROSINE-PHOSPHORYLATED PROTEINS THAT BIND TO GRB2.				
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CRK-I AND CRK-II (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THE CRK-I FORM LACKS THE LAST 100 RESIDUES.				
CC	-1- TISSUE SPECIFICITY: UBQUITOUS.				
CC	-1- DOMAIN: THE C-TERMINAL SH3 DOMAIN FUNCTION AS A NEGATIVE MODULATOR FOR TRANSFORMATION AND THE N-TERMINAL SH3 DOMAIN APPEARS TO FUNCTION AS A POSITIVE REGULATOR FOR TRANSFORMATION (BY SIMILARITY).				
CC	-1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.				
CC	-----				
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EMBL; S72408; AAB30755.1; -
DR PDB; 1CKA; 08-MAY-95.
DR PDB; 1CKB; 08-MAY-95.
DR PDB; 1B07; 06-JAN-99.
DR MGI; 88508; Crko.
DR InterPro; IPR000980; -
DR InterPro; IPR001452; -
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KW Phosphorylation; SH2 domain; SH3 domain; Alternative splicing;
KM Phosphorylation; 3D-structure.
FT DOMAIN 13 118 SH2.
FT DOMAIN 132 192 SH3.
FT DOMAIN 256 296 SH3.
FT VASPLC 205 304 MISSING (IN ISOFORM CRK-I).
SQ SEQUENCE 304 AA; 33814 MW; 5491896FC7A89065 CRC64;

Query Match 95.2%; Score 1612; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 4.2e-109; Mismatches 0; Indels 0; Gaps 0;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYMGRLSROEAVALLQGRHGVLFRDSTSPGDVLSVSENSRVSHYI 64
DB 2 AGNFDSEERSWYMGRLSROEAVALLQGRHGVLFRDSTSPGDVLSVSENSRVSHYI 61
QY 65 INSSGRRPPVPPSPAPPPGVSPSRIRIGDQFDSLPALLEFYKIHLYDTTLLIEPVARS 124
DB 62 INSSGRRPPVPPSPAPPPGVSPSRIRIGDQFDSLPALLEFYKIHLYDTTLLIEPVARS 121
QY 125 ROSSGVILROEAEYVRALFDNGNDEEDLPFKKGDILIRDKREEDQWMADESGKRG 184
DB 122 ROSSGVILROEAEYVRALFDNGNDEEDLPFKKGDILIRDKREEDQWMADESGKRG 181
QY 185 IPVPEYKRRPASASVSALLIGNQESHHPQLGPEPGPYAPSVNTPLPNLQNGPIYAR 244
DB 182 IPVPEYKRRPASASVSALLIGNQESHHPQLGPEPGPYAPSVNTPLPNLQNGPIYAR 241
QY 245 VIOKRVNAYDKTALALEVGLVYKTKINVSQWEGECNGKRGHPPTHVRLDQONPDE 304
DB 242 VIOKRVNAYDKTALALEVGLVYKTKINVSQWEGECNGKRGHPPTHVRLDQONPDE 301
QY 305 DFS 307
DB 302 DFS 304

RESULT 2
CRK_RAT
ID CRK_RAT STANDARD; PRT; 304 AA.
AC 063768;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCN-2000 (Rel. 40, Last annotation update)
DE PROTO-ONCOGENE C-CRK (P38) (ADAPTER MOLECULE CRK).
GN CRK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97057214; PubMed=8901553;

RA Kizaka-Kondoh S., Matsuda M., Okayama H.;
RT "CrkII signals from epidermal growth factor receptor to Ras";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12177-12182(1996).
CC -1- FUNCTION: THE CRK-I AND CRK-II FORMS DIFFER IN THEIR BIOLOGICAL
CC ACTIVITIES. CRK-II HAS LESS TRANSFORMING ACTIVITY THAN CRK-I. BOTH
CC CRK-I AND CRK-II BIND TO MANY OF TYROSINE-PHOSPHORYLATED PROTEINS
CC THAT BIND TO GRB2
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CRK-I AND CRK-II (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THE CRK-I FORM LACKS THE
CC LAST 100 RESIDUES.
CC -1- TISSUE SPECIFICITY: CRK-II IS EXPRESSED IN ALL TISSUES AND CELLS
CC WHEREAS CRK-I IS EXPRESSED AT LOWER LEVEL AND IN LIMITED CELL-
CC TYPES.
CC -1- DOMAIN: THE C-TERMINAL SH3 DOMAIN FUNCTION AS A NEGATIVE MODULATOR
CC FOR TRANSFORMATION AND THE N-TERMINAL SH3 DOMAIN APPEARS TO
CC FUNCTION AS A POSITIVE REGULATOR FOR TRANSFORMATION (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAINS.
CC
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DR EMBL; D44481; BAA07924.1; -
DR HSSP; Q64010; 1CKB.
DR InterPro; IPR000980; -
DR InterPro; IPR001452; -
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Proto-oncogene; SH2 domain; SH3 domain; Alternative splicing;
KM Phosphorylation.
FT DOMAIN 13 118 SH2.
FT DOMAIN 132 192 SH3.
FT DOMAIN 256 296 SH3.
FT VASPLC 205 304 MISSING (IN ISOFORM CRK-I).
FT VARIANT 244 244 Q -> R (NRK-23 INACTIVE MUTANT).
FT VARIANT 253 253 K -> E (NRK-23 INACTIVE MUTANT).
SQ SEQUENCE 304 AA; 33844 MW; 4CFBFB65BE72E265 CRC64;

Query Match 94.8%; Score 1605; DB 1; Length 304;
Best Local Similarity 99.3%; Pred. No. 1.3e-108; Mismatches 2; Indels 0; Gaps 0;
Matches 301; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYMGRLSROEAVALLQGRHGVLFRDSTSPGDVLSVSENSRVSHYI 64
DB 2 AGNFDSEERSWYMGRLSROEAVALLQGRHGVLFRDSTSPGDVLSVSENSRVSHYI 61
QY 65 INSSGRRPPVPPSPAPPPGVSPSRIRIGDQFDSLPALLEFYKIHLYDTTLLIEPVARS 124
DB 62 INSSGRRPPVPPSPAPPPGVSPSRIRIGDQFDSLPALLEFYKIHLYDTTLLIEPVARS 121
QY 125 ROSSGVILROEAEYVRALFDNGNDEEDLPFKKGDILIRDKREEDQWMADESGKRG 184
DB 122 ROSSGVILROEAEYVRALFDNGNDEEDLPFKKGDILIRDKREEDQWMADESGKRG 181
QY 185 IPVPEYKRRPASASVSALLIGNQESHHPQLGPEPGPYAPSVNTPLPNLQNGPIYAR 244
DB 182 IPVPEYKRRPASASVSALLIGNQESHHPQLGPEPGPYAPSVNTPLPNLQNGPIYAR 241
QY 245 VIOKRVNAYDKTALALEVGLVYKTKINVSQWEGECNGKRGHPPTHVRLDQONPDE 304
DB 242 VIOKRVNAYDKTALALEVGLVYKTKINVSQWEGECNGKRGHPPTHVRLDQONPDE 301

QY 305 DFS 307
 DB 302 DFS 304

RESULT 3
 CRK_HUMAN STANDARD: PRT; 304 AA.

AC P46108;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROTO-ONCOGENE C-CRK (P38) (ADAPTER MOLECULE CRK).
 GN CRK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic lung, and Placenta;
 RX MEDLINE=92334347; PubMed=1630456;
 RA Matsuda M., Tanaka S., Nagata S., Kojima A., Kurata T., Shibuya M.;
 RT "Two species of human CRK cDNA encode proteins with distinct
 RT biological activities."
 RL Mol. Cell. Biol. 12:3482-3489(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93390962; PubMed=8378094;
 RA Fioretos T., Heisterkamp N., Groffen J., Benjes S., Morris C.;
 RT "CRK proto-oncogene maps to human chromosome band 17p13."
 RL Oncogene 8:2853-2855(1993).
 CC -1- FUNCTION: THE CRK-I AND CRK-II FORMS DIFFER IN THEIR BIOLOGICAL
 CC ACTIVITIES. CRK-II HAS LESS TRANSFORMING ACTIVITY THAN CRK-I. BOTH
 CC CRK-I AND CRK-II BIND TO MANY OF TYROSINE-PHOSPHORYLATED PROTEINS
 CC THAT BIND TO GRB2.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CRK-I AND CRK-II (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THE CRK-I FORM LACKS THE
 CC LAST 100 RESIDUES.
 CC -1- DOMAIN: THE C-TERMINAL SH3 DOMAIN FUNCTION AS A NEGATIVE MODULATOR
 CC FOR TRANSFORMATION AND THE N-TERMINAL SH3 DOMAIN APPEARS TO
 CC FUNCTION AS A POSITIVE REGULATOR FOR TRANSFORMATION.
 CC -1- PTM: PHOSPHORYLATION OF CRK-II (40 KDA) GIVES RISE TO A 42 KDA
 CC FORM.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -----
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 CC -----
 CC EMBL: D10656; BAA01505.1; -;
 DR EMBL: S65701; AAB38213.1; -;
 DR HSSP: Q64010; ICKB.
 DR SWISS-2DPAGE; P46108; HUMAN.
 DR MIM: 164762; -;
 DR InterPro: IPR000980; -;
 DR InterPro: IPR001452; -;
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR PROTO-ONCOGENE; SH2 domain; SH3 domain; Alternative splicing;
 KW Phosphorylation.
 FT DOMAIN 13 118 SH2.
 FT DOMAIN 132 192 SH3.
 FT DOMAIN 256 296 SH3.

FT VARSPIC 205 304 MISSING (IN ISOFORM CRK-I).
 SQ SEQUENCE 304 AA; 33872 MW; D74A83ED1FC0EBC CRC64;
 Query Match 93.8%; Score 1588; DB 1; Length 304;
 Best Local Similarity 98.7%; Pred. No. 2,2e-107;
 Matches 299; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGNDESESRSSWYWGRLSRQEAVALLOGQRHGVFLVBDSTSPGDYVLSVENSRSVSHYI 64
 DB 2 AGNFSESRSSWYWGRLSRQEAVALLOGQRHGVFLVBDSTSPGDYVLSVENSRSVSHYI 61
 QY 65 INSSGPRPPVPPSPAPGPGVSPSRIRIGDQFDSLPALEFFYIHIHLDITTLIEPARS 124
 DB 62 INSSGPRPPVPPSPAPGPGVSPSRIRIGDQFDSLPALEFFYIHIHWDITTLIEPARS 121
 QY 125 ROGSGVILROEAEVYRALPFGNGNDEEDLPFKGDILRTIDKPEEOMWNAESEGKGM 184
 DB 122 ROGSGVILROEAEVYRALPFGNGNDEEDLPFKGDILRTIDKPEEOMWNAESEGKGM 181
 QY 185 IPVPYVEKYPASASVSALIGNEGSHPOPLGSGPEPGPYAOPSVNTPLPMLNGPIYAR 244
 DB 182 IPVPYVEKYPASASVSALIGNEGSHPOPLGSGPEPGPYAOPSVNTPLPMLNGPIYAR 241
 QY 245 VIQKRVPAVYKKTALALEVGVLYVYTKINVSQWEGECNGKRGHPTTHVRLDQNPDE 304
 DB 242 VIQKRVPAVYKKTALALEVGVLYVYTKINVSQWEGECNGKRGHPTTHVRLDQNPDE 301

QY 305 DFS 307
 DB 302 DFS 304

RESULT 4
 CRK_CHICK STANDARD: PRT; 305 AA.

AC Q04929;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PROTO-ONCOGENE C-CRK (P38).
 GN CRK.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93041379; PubMed=1329926;
 RA Reichman C.T., Mayer B.J., Khawer S., Hanafusa H.;
 RT "The product of the cellular crk gene consists primarily of SH2 and
 RT SH3 regions."
 RL Cell Growth Differ. 3:451-460(1992).
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -----
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 CC -----
 CC EMBL: L08168; AAA49001.1; -;
 DR HSSP: Q64010; ICKB.
 DR InterPro: IPR000980; -;
 DR InterPro: IPR001452; -;
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.

[illegible]

RA Mayer B.J., Hamaguchi M., Hanafusa H.;
 RT "A novel viral oncogene with structural similarity to phospholipase
 C.";
 RL Nature 332:272-275(1998).
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: Y00302; CAA68407.1; -
 DR PIR: A29851; A29851.
 DR PIR: B29851; TVPVI0.
 DR PIR: S00872; S00872.
 DR HSP: Q64010; ICKB.
 DR InterPro: IPR000980; -
 DR InterPro: IPR001452; -
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Oncogene; Polyprotein; SH3 domain; SH2 domain.
 FT DOMAIN 1 208 GAG.
 FT DOMAIN 209 437 CRK.
 FT DOMAIN 438 440 GAG.
 FT DOMAIN 248 354 SH2.
 FT DOMAIN 368 428 SH3.
 SQ SEQUENCE 440 AA; 47176 MW; 0DB543862E8982AC CRC64;

 Query Match 48.3%; Score 818.5; DB 1; Length 440;
 Best Local Similarity 77.3%; Pred. No. 6.8e-52;
 Matches 157; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

 QY 5 AGNDSEERSRWYGRSLRQENAVALLQGRHGFVLVNDSTSPQDYLVSYSENSRSHYI 64
 DB AGQDSDDRSRWYGRSLRQENAVALLQGRHGFVLVNDSTSPQDYLVSYSENSRSHYI 236
 QY 65 INSSGPPPPVPPSPAP-PPGVSPSPRLRIGDQEDSLPALLEPKYKHVLTPTLLIEPVAR 123
 DB VNSLGRPAGRRAGEGEGAGLNPTRFLIDQYFDSLPALLEPKYKHVLTPTLLIEPVSR 356
 QY 124 SRQSGVILRQEAEEYVRLDFNGNDEEDLPFRKGDILIRDKPEBOMNAEDSEGRK 183
 DB SRQSGVILRQEAEEYVRLDFNGNDEEDLPFRKGDILIRDKPEBOMNAEDSEGRK 416
 QY 184 MIPVYVEKRRPASASVALIG 206
 DB MIPVYVEKRRPASASVALIG 439

 RESULT 9
 CRK_DROME
 ID CRK_DROME STANDARD: PRT: 271 AA.
 AC G9XIM0;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ADAPTER MOLECULE CRK.
 GN CRK OR CG1587.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE-Embryo;
 RX MEDLINE=99173868; PubMed=10072777;
 RA Galletta B.J., Niu X.-P., Erickson M.R., Abmayr S.M.;
 RT "Identification of a Drosophila homologue to vertebrate Crk by
 RT interaction with MBC.";
 RL Gene 228:243-252(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
 RA Brannon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Broksstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheibel F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitsks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodde T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: ADAPTER PROTEIN WHICH INTERACTS WITH C-TERMINAL PORTION
 CC OF MBC. HOMOLOG OF HUMAN DOK180. MAY PLAY A ROLE IN CELLULAR
 CC PROCESSES THROUGHOUT DEVELOPMENT.
 CC -1- TISSUE SPECIFICITY: EMBRYONIC ZYGOTIC EXPRESSION IS SEEN IN
 CC IMAGINATING PRESUMPTIVE MESODERM AND ECTODERMALLY DERIVED TISSUES
 CC DURING GASTRULATION. AT STAGE 8, EXPRESSION IS ALSO SEEN IN
 CC ANTERIOR AND POSTERIOR MIDGUT AND CEPHALIC FURROW. BY STAGE 9,
 CC EXPRESSION IS HIGHEST IN VISCERAL MESODERM OF ANTERIOR AND
 CC POSTERIOR MIDGUT, VENTRAL NERVE CORD AND SOMATIC MESODERM.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
 CC THROUGHOUT EMBRYOGENESIS, DECLINES DURING LARVAL STAGES AND
 CC REAPPEARS DURING PUPATION.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -----
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 CC -----
 DR EMBL: AE003844; AAF59362.1; -

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DR EMBL: AF112976; AAD28428.1; -.
DR HSSP: Q64010; 1CKA.
DR FlyBase: FBgn0024811; Ctk.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SH2 domain; SH3 domain; Developmental protein.
KW DOMAIN 12 114 SH2.
FT DOMAIN 117 165 SH3.
FT DOMAIN 220 259 SH3.
SQ SEQUENCE 271 AA; 31205 MW; D1B4FE43150932DC CRC64;

Query Match 38.0%; Score 642.5; DB 1; Length 271;
Best Local Similarity 43.8%; Pred. No. 1.7e-39;
Matches 133; Conservative 42; Mismatches 68; Indels 61; Gaps 6;

QY 8 FDESESSWYMGRLSROEAVALLQGR-HGYFLVRSSTSPGCVLVSYSENSVHYIIN 66
   ||:||||:||||:|:| |||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 4 FVSDRSWYFGPMRQDATEVLMNERGVFLVRSNSTAGDYLCVREDTFVSNYIIN 63

QY 67 SSGPRPPVPPSPAQPPGVSPSRLRIGDQEFDSLPALEFYKIHVLTDTTLLEPVARSQ 126
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 64 KVOQOQOIV-----YRIGDOSFDLPRLKILFTYLAHTDTTPPKRPACR--- 106

QY 127 GSGVILLROEAEYRALFDENGDEEDLPFKGDLIRIDKPEEQWMAEDSGKRGMP 186
   -|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 107 -----RVEKVIKGFDEVGSDODDLPQGRGEVLTIVAKDDQWMTARNSSGKIGQIP 157

QY 187 VEVYERY-----RPAASVSLIGNQBGSHQPLGCGPPRPGYACQSVNTPPLP 234
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 158 VPTQDDYDMDDAIDKNEPSSISGSNVFESTLK-----RDLNRKLI- 200

QY 235 NLONGPIYAVIQRVPNAVDTALALEVGLVKTAKINVGQMEGECNGKRGHPFTHY 294
   | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 201 ----PAYAVKQSRVPNATKALKEIGDIIKVTKTNTINGQWBEELNGKNHFFFTHY 255

QY 295 RLID 298
   :|
DB 256 EFVD 259

RESULT 10
GRAP_HUMAN STANDARD; PRT; 217 AA.
AC 013588;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GKB2-RELATED ADAPTOR PROTEIN.
GN GRAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96218119; PubMed=8647802;
RA Peng G.-S., Ouyang Y.-B., Hu D.-P., Shi Z.-Q., Gentz R., Ni J.;
RT "Grp is a novel SH3-SH2-SH3 adaptor protein that couples tyrosine
RT kinases to the Ras pathway.";
RL J. Biol. Chem. 271:12129-12132(1996).
CC -|- FUNCTION: COUPLE SIGNALS FROM RECEPTOR AND CYTOPLASMIC TYROSINE
CC KINASES TO THE RAS SIGNALING PATHWAY.
CC -|- SUBUNIT: ASSOCIATES THROUGH ITS SH2 DOMAIN WITH LIGAND-ACTIVATED
CC RECEPTORS FOR STEM CELL FACTOR (KIT) AND ERYTHROPOIETIN (EPOR).
CC ALSO FORMS A STABLE COMPLEX WITH THE BCR-ABL ONCOPROTEIN. GRAP IS
CC ASSOCIATED WITH THE RAS GUANINE NUCLEOTIDE EXCHANGE FACTOR SOS1,
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```
CC PRIMARILY THROUGH ITS N-TERMINAL SH3 DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -|- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -|- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
-----
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CC EMBL: U52518; AAC50541.1; -.
DR MIM: 604330; -.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 2.
KW SH2 domain; SH3 domain.
FT DOMAIN 1 58 SH3.
FT DOMAIN 60 152 SH2.
FT DOMAIN 156 215 SH3.
SQ SEQUENCE 217 AA; 25336 MW; 09FEC2F3BAC0FAF8 CRC64;

Query Match 15.2%; Score 257; DB 1; Length 217;
Best Local Similarity 31.4%; Pred. No. 6.4e-12;
Matches 64; Conservative 40; Mismatches 54; Indels 46; Gaps 9;

QY 2 RGCAG----NFDSESSWYMGRLSROEAVALLQGRH-GVFLVRSSTSPGCVLVSYSE 56
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 42 RVEGEFIPKNTYRVRPHRYSGRISRLQAEELMRNHLGAFILRESSSGCEFSVSNY 101

QY 57 NSRVSHYII--NSSGPRPPVPPSPAQPPGVSPSRLRIGDQEFDSLPALEFYKIHVLT 114
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 102 GQOVQHFVKVLRBASG-----KYFLMEEKFNLSNLTVDYFR-----T 137

QY 115 TTLLEPVARSRGSGVILLROE-----AEYRALFDPNGDEEDLPFKGDLIRIDK 167
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 138 TT----IARKRQ--IFLDEEPLKSPACFPAQAFDSADPSQLSFRGDIILEVLR 190

QY 168 PEOQWMAEDSEKRGKMPVPYVE 191
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 191 PDPHMRGR-SCGRVGFPPRSTVQ 213

RESULT 11
DRK_DROME STANDARD; PRT; 211 AA.
AC 008012; Q9Y605;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN K(Sev)2B (SH2-SH3 ADAPTER PROTEIN DRK).
GN DRK OR E(Sev)2B OR CG6033.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUB=Eye;
RX MEDLINE=93214989; PubMed=8462097;
RA Simon M.A., Dodson G.S., Rubin G.M.;
RT "Ain SH3-SH2-SH3 protein is required for p21Ras1 activation and binds
RT to sevenless and Sos proteins in vitro.";
RL Cell 73:169-177(1993).
RN [2]
```


RT libraries.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9015-9019(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES-Rat; STRAIN-Wistar; TISSUE-Brain;
 RX MEDLINE-95293967; PubMed-775428;
 RA Watanabe K., Fukuchi T., Hosoya H., Shirasawa T., Matsuo K.,
 RA Miki H., Takenawa T.;
 RT "Splicing isoforms of rat Ash/Grb2. Isolation and characterization of
 RT the cDNA and genomic DNA clones and implications for the
 RT physiological roles of the isoforms.";
 RL J. Biol. Chem. 270:13733-13739(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM GRB2-3).
 RC SPECIES-Human; TISSUE-Placenta;
 RX MEDLINE-94233382; PubMed-8178156;
 RA Path I., Schweighoffer F., Rey I., Multon M.C., Boiziau J.,
 RA Duchesne M., Tocque B.;
 RT "Cloning of a Grb2 isoform with apoptotic properties.";
 RL Science 264:971-974(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human; TISSUE-Epidermis;
 RX MEDLINE-99162407; PubMed-10051406;
 RA Boemann H., Gehrisch S., Jaross W.;
 RT "The gene structure of the human growth factor bound protein GRB2.";
 RL Genomics 56:203-207(1999).
 RN [6]
 RP ASSOCIATION WITH IRS-1.
 RX MEDLINE-93265568; PubMed-8388384;
 RA Tobe K., Matuoka K., Tamemoto H., Ueki K., Kaburagi Y., Asai S.,
 RA Noguchi T., Matsuda M., Tanaka S., Hattori S., Fukui Y., Akanuma Y.,
 RA Yuzaki Y., Takenawa T., Kadowaki T.;
 RT "Insulin stimulates association of insulin receptor substrate-1 with
 RT the protein abundant Src homology/growth factor receptor-bound
 RT protein 2.";
 RL J. Biol. Chem. 268:11167-11171(1993).
 RN [7]
 RP ASSOCIATION WITH IRS-1 AND SHC.
 RX MEDLINE-93259135; PubMed-8491186;
 RA Scolnik E.Y., Lee C.-H., Batzer A., Vicentini L.M., Zhou M., Daly R.,
 RA Myers M.J., Jr., Backer J.M., Ullrich A., White M.F., Schlessinger J.;
 RT "The SH2/SH3 domain-containing protein GRB2 interacts with tyrosine-
 RT phosphorylated IRS1 and Shc: implications for insulin control of ras
 RT signaling.";
 RL EMBO J. 12:1929-1936(1993).
 RN [8]
 RP STRUCTURE BY NMR OF 1-56.
 RX MEDLINE-97280795; PubMed-9135122;
 RA Wittekind M., Mepelli C., Lee V., Goldfarb V., Friedrichs M.S.,
 RA Meyers C.A., Mueller L.;
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with
 RT a ten-residue peptide derived from SOS: direct refinement against
 RT NOES, J-couplings and 1H and 13C chemical shifts.";
 RL J. Mol. Biol. 267:933-952(1997).
 RN [9]
 RP STRUCTURE BY NMR OF 60-158.
 RX MEDLINE-96387228; PubMed-8794768;
 RA Thornton K.H., Mueller W.T., McConnell P., Zhu G., Saltiel A.R.,
 RA Thanabal V.;
 RT "Nuclear magnetic resonance solution structure of the growth factor
 RT receptor-bound protein 2 Src homology 2 domain.";
 RL Biochemistry 35:11852-11864(1996).
 RN [10]
 RP STRUCTURE BY NMR OF 53-163.
 RA Senior M.M., Frederick A.F., Black S., Perkins L.M., Wilson O.,
 RA Snow M.E., Wang Y.-S.;
 RL Submitted (JUN-1997) to the PDB data bank.
 RN [11]
 RP STRUCTURE BY NMR OF 159-215.
 RX MEDLINE-95187706; PubMed-7881903;
 RA Konda D., Terasawa H., Ichikawa S., Ogura K., Hatanaka H.,
 RA Mandiyan V., Ullrich A., Schlessinger J., Inagaki F.;

RT "Solution structure and ligand-binding site of the carboxy-terminal
 RT SH3 domain of GRB2.";
 RL Structure 2:1029-1040(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).
 RX MEDLINE-95232505; PubMed-7716522;
 RA Maignan S., Guilloteau J.P., Fromage N., Arnoux B., Bequart J.,
 RA Ducruix A.;
 RT "Crystal structure of the mammalian Grb2 adaptor.";
 RL Science 268:291-295(1995).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 56-153.
 RX MEDLINE-98308003; PubMed-9642078;
 RA Rahnel J., Garcia-Echeverria C., Furet P., Strauss A., Caravatti G.,
 RA Fretz H., Schoepfer J., Gay B.;
 RT "Structural basis for the high affinity of amino-aromatic SH2
 RT phosphopeptide ligands.";
 RL J. Mol. Biol. 279:103-1022(1998).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 49-163.
 RX MEDLINE-99192587; PubMed-10090780;
 RA Elmayer P., France D., Gounarides J., Jarosinski M., Martin M.-S.,
 RA Rondeau J.-M., Sabio M., Topiol S., Weidmann B., Zurini M., Bair K.W.;
 RT "Structural and conformational requirements for high-affinity binding
 RT to the SH2 domain of Grb2(1).";
 RL J. Med. Chem. 42:971-980(1999).
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK; PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -1- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING
 CC PROLIFERATIVE SIGNALS, MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH.
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
 CC -----
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 CC -----
 DR EMBL: M96995; AAA58448.1; -
 DR EMBL: X62852; CAA44664.1; -
 DR EMBL: X62853; CAA44665.1; -
 DR EMBL: D49846; BAA08645.1; -
 DR EMBL: L29511; AAC37549.1; -
 DR EMBL: AF063618; AAC72075.1; -
 DR EMBL: AF063614; AAC72075.1; JOINED.
 DR EMBL: AF063615; AAC72075.1; JOINED.
 DR EMBL: AF063616; AAC72075.1; JOINED.
 DR EMBL: AF063617; AAC72075.1; JOINED.
 DR PIR: AA3321; A43321.
 DR PIR: S26050; S26050.
 DR PDB: 1GRI; 08-MAR-96.
 DR PDB: 1GRC; 31-AUG-94.
 DR PDB: 1GFD; 31-AUG-94.

DR PDB; 1GHU; 27-JAN-97.
 DR PDB; 1TZE; 07-JUL-97.
 DR PDB; 1FHS; 17-JUN-98.
 DR PDB; 1BM2; 05-AUG-98.
 DR PDB; 1BMB; 29-JUL-98.
 DR PDB; 1ZEP; 30-MAR-99.
 DR MIM; 108355; -.
 DR InterPro; IPR000980; -.
 DR InterPro; IPR001452; -.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PROSITE; PSS0001; SH2; 1.
 DR PROSITE; PSS0002; SH3; 2.
 DR SH2 domain; SH3 domain; Alternative splicing; 3D-structure.
 FT DOMAIN 1 58 SH3.
 FT DOMAIN 60 152 SH2.
 FT DOMAIN 156 215 SH3.
 FT VARSPIC 60 100 MISSING (IN ISOFORM GRB3-3).
 FT VARSPIC 157 170 MISSING (IN ISOFORM ASH-M).
 FT MUTAGEN 49 49 P->L: INEFFECTIVE IN DNA SYNTHESIS.
 FT MUTAGEN 203 203 G->R: INEFFECTIVE IN DNA SYNTHESIS.
 SQ SEQUENCE 217 AA; 25206 MW; 83A4B0BA1B248DC4 CRC64;

Query Match 13.2%; Score 224; DB 1; Length 217;
 Best Local Similarity 27.9%; Pred. No. 1.5e-09;
 Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSESSSWYGRSLRQEAVALLOGRH-GVFLYRDSSTSPGDYLVSENSRVSHYII 65
 DB 51 NIEKMPHFMPFGKIPRAKAEMLSKQRHDGAFILIRESEADPSLSYKFGNDVQHFVY 110
 QY 66 NSSGPRPVPPAPDPPVSPSLRIGQEDPSLPALIEFKIHYLDTTLIEPVARS 125
 DB 111 LRDG-----AGKFLWYVKNLSLNEIDYHR-----STS---VSRNQ 144
 QY 126 QGSGVILRG-----EEAYVALPFGNDEDDLPFKKGDILIRDKPEEQWMAEDSEG 180
 DB 145 Q---IFRLIEGVPOQPTVYQALFEPDPEDELGFRRDQFHVMDNSDPNMWKA-CHG 200
 QY 181 KRGKTPVPVY 190
 DB 201 QRGMEPRNVY 210

RESULT 13
 GRB2_MOUSE STANDARD; PRT: 217 AA.
 ID GRB2_MOUSE
 AC Q60631; Q61240;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTER PROTEIN)
 DE (SH2/SH3 ADAPTER GRB2).
 GN GRB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=93360985; Pubmed=7689150;
 RA "Suen K., Bustelo X.R., Pawson T., Barbacid M.:
 RT "Molecular cloning of the mouse grb2 gene: differential interaction
 RT of the Grb2 adaptor protein with epidermal growth factor and nerve
 RT growth factor receptors.";
 RL Mol. Cell. Biol. 13:5500-5512(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM GRB3-3).
 RC STRAIN-BALB/C;

RA Tanaka S.;
 RN Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP STRUCTURE BY NMR OF 1-59.
 RX MEDLINE=97280795; Pubmed=9135122;
 RA Wittekand M., Kapell C., Lee V., Goldfarb V., Friedrichs M.S.,
 RA Meyers C.A., Mueller L.;
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with
 RT a ten-residue peptide derived from SOS: direct refinement against
 RT NOES, J-couplings and 1H and 13C chemical shifts.";
 RL J. Mol. Biol. 267:933-952(1997).
 CC -I- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -I- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -I- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING
 CC PROLIFERATIVE SIGNALS, MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH
 CC (BY SIMILARITY).
 CC -I- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -I- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U07617; AAB40022.1; -.
 CC EMBL; D85748; BAA12862.1; -.
 DR PDB; 1GBQ; 04-SEP-97.
 DR PDB; 2GBQ; 04-SEP-97.
 DR PDB; 3GBQ; 04-SEP-97.
 DR PDB; 4GBQ; 04-SEP-97.
 DR PDB; 1GBR; 26-JAN-95.
 DR MGD; MGI:95805; Grb2.
 DR InterPro; IPR000980; -.
 DR InterPro; IPR001452; -.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PROSITE; PSS0001; SH2; 1.
 DR PROSITE; PSS0002; SH3; 2.
 KW SH2 domain; SH3 domain; Alternative splicing; 3D-structure.
 FT DOMAIN 1 58 SH3.
 FT DOMAIN 60 152 SH2.
 FT VARSPIC 60 100 MISSING (IN ISOFORM GRB3-3).
 SQ SEQUENCE 217 AA; 25238 MW; 97FAA4FB4B248DDF CRC64;

Query Match 13.2%; Score 224; DB 1; Length 217;
 Best Local Similarity 27.9%; Pred. No. 1.5e-09;
 Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSESSSWYGRSLRQEAVALLOGRH-GVFLYRDSSTSPGDYLVSENSRVSHYII 65
 DB 51 NIEKMPHFMPFGKIPRAKAEMLSKQRHDGAFILIRESEADPSLSYKFGNDVQHFVY 110
 QY 66 NSSGPRPVPPAPDPPVSPSLRIGQEDPSLPALIEFKIHYLDTTLIEPVARS 125
 DB 111 LRDG-----AGKFLWYVKNLSLNEIDYHR-----STS---VSRNQ 144
 QY 126 QGSGVILRG-----EEAYVALPFGNDEDDLPFKKGDILIRDKPEEQWMAEDSEG 180
 DB 145 Q---IFRLIEGVPOQPTVYQALFEPDPEDELGFRRDQFHVMDNSDPNMWKA-CHG 200
 QY 181 KRGKTPVPVY 190
 DB 201 QRGMEPRNVY 210

Db 51 NYIEMKPHWPFEGKIPRAKAEMLSKQRHDAFLIRESEAPGDSLSVKFGNDVOHFXY 110
 QY 66 NSSGPRPVPPSPAPPPGVSPSRLRIGDQFDSLPALEFYKIHVDTTLLIEPVARSR 125
 Db 111 LRDS-----AGKYLWVVKFNSLNELVDYHR-----STS-----YSRNO 144
 QY 126 QGSGVILRQ-----EEAEYRALFPDNGNDEEDLPFKKGDIILIRDKPEEOMNAEDSEG 180
 Db 145 Q---IFLRDIEGVPOQPTVYQALFDPQEGELGFRGDFIYHMDNSDPMMWKA-CHG 200
 QY 181 KRGMTPVPYV 190
 Db 201 QTGMFPRNTV 210

RESULT 14
 GRB2.CHICK STANDARD; PRT; 217 AA.
 AC 007883;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTER PROTEIN)
 DE (SH2/SH3 ADAPTER GRB2) (ASH PROTEIN).
 GN GRB2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94085795; PubMed=8262390;
 RA Masenius V.-M., Merilainen J., Lehto V.-P.;
 RT "Sequence of a chicken cDNA encoding a Grb2 protein.";
 RL Gene 134:299-300(1993).
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
 CC -----
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 CC -----
 CC EMBL; L19258; AAA16318.1; -.
 DR PIR; J70664; J70664.
 DR HSSP; P29354; 1GRI.
 DR InterPro; IPR000980; -.
 DR InterPro; IPR001452; -.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00452; SHADOMAIN.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW SH2 domain; SH3 domain.

FT DOMAIN 1 58 SH3.
 FT DOMAIN 60 152 SH2.
 FT DOMAIN 156 215 SH3.
 SQ SEQUENCE 217 AA; 25076 MW; DDC9A84ECD52859 CRC64;
 Query Match 12.9%; Score 218; DB 1; Length 217;
 Best Local Similarity 27.9%; Pred. No. 4,1e-09;
 Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;
 QY 7 NFDSEERSWYMGRLSROAVALLQGRH-GVEIYRDSSTSPGQVYLSVSENSRSHYII 65
 Db 51 NYIEMKPHWPFEGKIPRAKAEMLSKQRHDAFLIRESEAPGDSLSVKFGNDVOHFXY 110
 QY 66 NSSGPRPVPPSPAPPPGVSPSRLRIGDQFDSLPALEFYKIHVDTTLLIEPVARSR 125
 Db 111 LRDS-----AGKYLWVVKFNSLNELVDYHR-----STS-----YSRNO 144
 QY 126 QGSGVILRQ-----EEAEYRALFPDNGNDEEDLPFKKGDIILIRDKPEEOMNAEDSEG 180
 Db 145 Q---IFLRDIEGVPOQPTVYQALFDPQEGELGFRGDFIYHMDNSDPMMWKA-CHG 200
 QY 181 KRGMTPVPYV 190
 Db 201 QTGMFPRNTV 210

RESULT 15
 GRB2.XENLA STANDARD; PRT; 217 AA.
 ID GRB2.XENLA
 AC P87379;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2 ADAPTER PROTEIN)
 DE (SH2/SH3 ADAPTER GRB2).
 GN GRB2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu W., Mayer B.J.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC PROTEINS IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS (BY
 CC SIMILARITY).
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
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 CC -----
 CC EMBL; U89775; AAA49699.1; -.
 DR InterPro; IPR000980; -.
 DR InterPro; IPR001452; -.

DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 2.
KW SH2 domain; SH3 domain.
FT DOMAIN 1 58 SH3.
FT DOMAIN 60 152 SH2.
FT DOMAIN 156 215 SH3.
SQ SEQUENCE 217 AA; 25104 MW; 1622802ED26CE46A CRC64;

Query Match 12.68; Score 214; DB 1; Length 217;
Best Local Similarity 28.48; Pred. No. 7.9e-09;
Matches 54; Conservative 44; Mismatches 56; Indels 36; Gaps 8;
QY 7 NFDSEERSWYGRSLROEAVALLQGRH-GVFLVRODSTSPGDVVLVSSENSRVSHYII 65
DB 51 NIEMKAHPWTFGKIIPRAKAEMLGKQKHDAFLIRESESAPGDFSLSVKFGNDVQHFKV 110
QY 66 NSSGPRPPVPPSPAPPPQGVSPSRLRIGDQEFDSLALLEEYKTIHYLDTTTLIEPVARSR 125
DB 111 -----LPDGACKYFLMV--VKFNSINELVDYHR-----STS---VSRNQ 144
QY 126 QGSGVILRQ----EEAEYVRALPDENGNDDEDLPKKGDILRIIDKPEEQMNAEDSEG 180
DB 145 Q--IFLRDIEOVPOQPTYVQALFDQDPEQDGLGFRNGDFTIYVVDNSDPNMWKG-TCLS 200
QY 181 KRGMIIPVPYV 190
DB 201 QTGMFPRNYV 210

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